Amendments to the Specification

Please replace paragraph [0053] with the following paragraph:

[0054] 5'- GCCTGTTGTGAGCCTCCTGTCGAA -(N_{40})- TTGAGCGTTTATTCTTGTCTCCCTATAGTGAGTCGTATTA -3' (SEQ ID NO:1) is synthesized using an ABI EXPEDITE™ DNA synthesizer, and purified by standard methods (N_{40} denotes a random sequence of 40 nucleotides built uniquely into each aptamer). Approximately 10^{15} DNA molecules with unique sequences from the template pool can be PCR amplified using the primers YW.42.30.A (5'-TAATACGACTCACTATAGGGAGACAAGAATAAACGCTCAA-3') (SEQ ID NO:2) and YW.42.30B (5'-GCCTGTTGTGAGCCTCCTGTCGAA-3') (SEQ ID NO:3). Amplified pool PCR product is precipitated with ethanol, re-suspended in water and desalted on a Nap-5 column (Pharmacia). Approximately 4 x 10^{15} DNA molecules from the pool PCR amplification are transcribed *in vitro* using a mutant Y639F T7 RNA polymerase which accepts 2'-fluoropyrimidines (Sousa, 1999), 2'-fluoropyrimidine and 2'-OH purine NTPs, to yield ~3 x 10^{16} RNA molecules with corresponding sequences. Stabilized 2'-fluoro-pyrimidine pools made up of 10^{14}-10^{15} random sequences in a total volume of approximately 100 µl are contacted with either biotinylated target immobilized in neutravidin coated plates (Pierce) or adherent target-expressing cells immobilized in plates. A typical binding buffer used for the positive and negative selection steps contains 20 mM HEPES, pH 7.4, 150 mM NaCl, 10 mM MgCl2, 1 mM EDTA, 1 mM DTT, and 0.1 mg/ml tRNA (4 mM). Following a 10 min. negative incubation step at room temperature, RNAs which bind to the target alone will be removed in this negative selection step. The solution containing unbound RNA is then transferred to another identical well containing immobilized target and effector is added to the solution. The concentration of effector added can be adjusted to ultimately enrich molecules which respond to effector at the most appropriate concentration. Initially the effector is provided at saturating concentrations (typically millimolar for small molecule effectors such as glucose and high micromolar concentration for protein effectors) to ensure that molecules with any measure of effector dependence are isolated. In successive rounds of selection, the effector concentration can be reduced to preferentially isolate the most effector-dependent molecules. Following an

equilibration period of 1 hour, wells are rinsed with excess binding buffer (typically washing four times with 120ul of 1x ASB on a robotic plate washer with 30 sec. shakes). 50 µl of RT mix (RT primer, 4µM; 5x "Thermo buffer", 1x; DTT, 100 mM; mixed dNTPs, 0.2mM each; vanadate nucleotide inhibitor 200µM; tRNA 10µg/ml; 0.5µl Invitrogen Thermoscript Reverse Transcriptase; brought to 50 µl with water) is added to the selection well and incubated at 65°C for 30 min with tape over wells to reduce evaporation.

Please replace paragraph [0115] with the following paragraph:

[0115] Fpg activity assays were carried out at room temperature in 1 x SB under steady-state conditions with 1 nM Fpg. An 18-mer dsDNA was used as the Fpg substrate. The 8-oxo-dG-containing strand was 5' labeled and had the following sequence; d(5'-TCATGG GTC(8-oxo-G)TCGGTATA-3') (SEQ ID NO:4), and the complementary strand contained a cytidine opposite 8-oxo-dG. Reaction components were mixed in 18 µl and incubated for 12 min, followed by the addition of 2 µ1 of 200 nM DNA substrate (20 nM final). After 7 min, reactions were quenched with 15 µl of 95°C stop solution (97% formamide, 0.02% xylene cyanol in 0.2x TBE) and heated at 95°C for an additional 5 mm. The reactions were resolved on 15% denaturing PAGE and visualized using phosphorimager screens. The amount of product was calculated as a percent of 20 nM substrate and without any inhibitors was measured to be approximately 2 nM under these conditions.

Please insert the sequence listing, pages 1 – 2, at the end of the specification.

Applicants submit a Sequence Listing for the nucleotide sequences and amino acid sequences disclosed in the specification in compliance with the requirements for patent applications containing nucleotide sequences and/or amino acid sequence disclosures. 37 C.F.R. §§ 1.821-1.825.

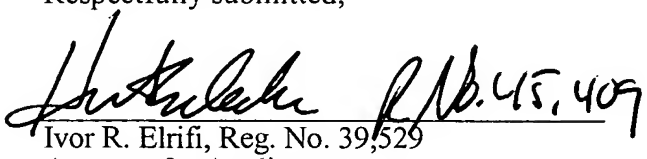
Applicants believe no fees are due in connection with this filing. Please charge any additional fees that may be due, or credit any overpayment of same, to Deposit Account No. 50-0311, Reference No. 23239-537.

CONCLUSION

On the basis of the foregoing amendment and remarks, Applicants respectfully submit, that the pending claims are in condition for allowance. If there are any questions regarding this amendment and remark, the Examiner is encouraged to contact the undersigned at the telephone number provided below.

Dated: January 23, 2004

Respectfully submitted,



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